

Appl. No. : 10/035,978  
Filed : December 21, 2001

## REMARKS

In Response to the Office Action of January 29, 2004, Applicants have amended claim 14 which now recites the elected sequence, SEQ ID NO: 126. All remaining claims depend ultimately from claim 14. Consequently, Applicants assert that the remaining claims may be properly rejoined and allowed to proceed to issue.

Claims 3-4 and 20-23 have been cancelled. Claims 1, 9, 10, 13, 14, 15, 17, and 24 have been amended. Claims 1-2, 5-19 and 24 are now pending in this application. Support for the amendments is found in the existing claims and the specification as discussed below. Accordingly, the amendments do not constitute the addition of new matter.

### Sequence rules

The Examiner asserts that the application fails to comply with the sequence rules because the specification contains sequences that are not identified by SEQ ID NO. In response, the specification describes the sequences by SEQ ID NO throughout the specification. See particularly pages 12-17, 21, and 33-35. In particular, primers and probes are summarized in Tables 1 and 2 on pages 44-46 of the present specification. Specifically, the sequences of page 32, lines 21-22 are identified in Table 1, page 44. The sequences of page 37, Table 3 are identified in Table 1, page 44. The sequences of page 38, lines 17-18 are identified in Table 2, pages 45-46. The sequences of page 39, Table 4 are identified in Table 1, page 44. The sequences of page 40, Table 5 are identified in Table 2, pages 45-46. The sequences of page 42, Table 6 are identified in Table 2, pages 45-46. Consequently, all of the sequences in the specification are identified by SEQ ID NO. The sequences not identified in the text are identified in the two Tables, Tables 1-2 of pages 44-46 of the present specification. The Examiner is respectfully requested to point out specifically any sequences which are not identified by SEQ ID NO.

The Examiner also states that it is not clear if SEQ ID NOS: 126 & 127 are intended to be identical in length and sequence. Applicant responds that SEQ ID NOS: 126 & 127 are indeed identical but were given two different SEQ ID NOS because they are from two different isolates, HK43001 (SEQ ID NO: 126) and N3001 (SEQ ID NO: 127).

In view of the remarks above, Applicants submit that the present application is in compliance with the sequence rules.

### Information Disclosure Statement

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The Office Action states that the listing on pages 47-48 of the specification is not a proper Information Disclosure Statement and has not been considered by the Examiner. Applicants respond that the references listed on pages 47 and 48 merely provide bibliographic information for the discussion on pages 1 and 2 of the specification and are not intended as an Information Disclosure Statement.

**Abstract**

A substitute Abstract on a separate sheet is submitted herewith.

**Allowable subject matter**

Applicants gratefully acknowledge the indication of allowable subject matter for SEQ ID NO: 126. With this amendment, Applicants have amended claim 14 accordingly and have made all of the outstanding claims dependent upon claim 14. Support for the amendment to claims 1, 9, and 15 is found in paragraphs 0078, 0236 and Figure 12 (sheets 27, 30, and 33) of the published application. Note that SEQ ID NO: 126 corresponds to the s1c sequence from isolate HK43001.

In view of Applicants' amendments, rejoinder and allowance of claims 1-2, 5-19 and 24 is respectfully requested.

**CONCLUSION**

In view of Applicants' amendments to the claims and the foregoing Remarks, it is respectfully submitted that the present application is in condition for allowance. Should the Examiner have any remaining concerns which might prevent the prompt allowance of the application, the Examiner is respectfully invited to contact the undersigned at the telephone number appearing below.

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Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

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Dated: July 22, 2004

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## PROBES, METHODS AND KITS FOR DETECTION AND TYPING OF HELICOBACTER PYLORI NUCLEIC ACIDS IN BIOLOGICAL SAMPLES

### Abstract of the Disclosure

The present invention relates to a method for the detection and/or typing of *Helicobacter pylori* strains present in a sample. The method includes the steps of amplifying particular regions of the *vacA* gene and other virulence determinant genes and hybridization for allele-specific detection of a strain according to the virulence determinant gene alleles present in the particular *H. pylori* strain. Probes and primers for carrying out the method are also disclosed.